

SUBSTITUTE SEQUENCE LISTING

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<120> Cyanide-tolerant nitrile hydratases

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<140> US/10/598,873

<141> 2006-09-14

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<170> PatentIn version 3.3

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<223> Coding region of alpha-subunit gene

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<221> gene

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Glu Arg Ala Trp Ala Leu Phe Gln Val Leu Lys Ser Lys Glu Leu Ile
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99

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Pro Glu Gly Tyr Val Glu Gln Leu Thr Gln Leu Met Glu His Gly Trp
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147

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195

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243

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291

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cac cgc acg tca gag aaa tgg ccg ttc ccc gac gca atc ggg cat ggc His Arg Thr Ser Glu Lys Trp Pro Phe Pro Asp Ala Ile Gly His Gly 350	355	360	1162
gat gta agc gca gcc cat caa ccc acc tac cac gtc gag ttc gcc gtg Asp Val Ser Ala Ala His Gln Pro Thr Tyr His Val Glu Phe Ala Val 370	375	380	1210
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Val Val Ala Lys Ala Trp Val Asp Pro Gln Phe Arg Ala Leu Leu Leu
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Lys Asp Gly Thr Ala Ala Cys Ala Gln Phe Gly Tyr Thr Gly Pro Gln
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Ile Val Cys Ser Leu Cys Ser Cys Thr Asn Trp Pro Val Leu Gly Leu
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Pro Pro Glu Trp Tyr Lys Gly Phe Glu Phe Arg Ala Arg Leu Val Arg
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Val Gly

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Lys Lys Phe Ser Val Asp Glu Val Arg His Ala Val Glu Arg Leu Asp
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90

95

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Gly Asp Cys Arg Gln Glu Leu Val Phe Ile Gly Gln Gly Leu Asp Thr																																			
355	360		365	gac gcg tta cag cgc gag ctc gac cac tgc ctg agc gcc cag gaa	1152	Asp Ala Leu Gln Arg Glu Leu Asp His Cys Leu Leu Ser Ala Gln Glu		370	375		380	atc gcc gcc ggc cca ctg gcc tgg caa gcg ctg cca ggg gcg acc gcc	1200	Ile Ala Ala Gly Pro Leu Ala Trp Gln Ala Leu Pro Gly Ala Thr Ala		385	390		395		400	ttt gac cga cag acc ctt gcc cgc ccc cca cac agc cca tgg cga ttg	1248	Phe Asp Arg Gln Thr Leu Ala Arg Pro Pro His Ser Pro Trp Arg Leu		405	410		415	ccc cca ttt gat ccg aga tag	1269	Pro Pro Phe Asp Pro Arg		420	
	365																																		
gac gcg tta cag cgc gag ctc gac cac tgc ctg agc gcc cag gaa	1152																																		
Asp Ala Leu Gln Arg Glu Leu Asp His Cys Leu Leu Ser Ala Gln Glu																																			
370	375		380	atc gcc gcc ggc cca ctg gcc tgg caa gcg ctg cca ggg gcg acc gcc	1200	Ile Ala Ala Gly Pro Leu Ala Trp Gln Ala Leu Pro Gly Ala Thr Ala		385	390		395		400	ttt gac cga cag acc ctt gcc cgc ccc cca cac agc cca tgg cga ttg	1248	Phe Asp Arg Gln Thr Leu Ala Arg Pro Pro His Ser Pro Trp Arg Leu		405	410		415	ccc cca ttt gat ccg aga tag	1269	Pro Pro Phe Asp Pro Arg		420									
	380																																		
atc gcc gcc ggc cca ctg gcc tgg caa gcg ctg cca ggg gcg acc gcc	1200																																		
Ile Ala Ala Gly Pro Leu Ala Trp Gln Ala Leu Pro Gly Ala Thr Ala																																			
385	390		395		400	ttt gac cga cag acc ctt gcc cgc ccc cca cac agc cca tgg cga ttg	1248	Phe Asp Arg Gln Thr Leu Ala Arg Pro Pro His Ser Pro Trp Arg Leu		405	410		415	ccc cca ttt gat ccg aga tag	1269	Pro Pro Phe Asp Pro Arg		420																	
	395		400	ttt gac cga cag acc ctt gcc cgc ccc cca cac agc cca tgg cga ttg	1248	Phe Asp Arg Gln Thr Leu Ala Arg Pro Pro His Ser Pro Trp Arg Leu		405	410		415	ccc cca ttt gat ccg aga tag	1269	Pro Pro Phe Asp Pro Arg		420																			
	400																																		
ttt gac cga cag acc ctt gcc cgc ccc cca cac agc cca tgg cga ttg	1248																																		
Phe Asp Arg Gln Thr Leu Ala Arg Pro Pro His Ser Pro Trp Arg Leu																																			
405	410		415	ccc cca ttt gat ccg aga tag	1269	Pro Pro Phe Asp Pro Arg		420																											
	415																																		
ccc cca ttt gat ccg aga tag	1269																																		
Pro Pro Phe Asp Pro Arg																																			
420																																			

<210> 5
<211> 422
<212> PRT
<213> Pseudomonas marginalis

<400> 5

Met Thr Asp Gly Ala Gln Ala Ser Arg Leu Pro Val Thr Val Leu Ser
1 5 10 15

Gly Phe Leu Gly Ala Gly Lys Thr Thr Leu Leu Asn His Ile Leu Arg
20 25 30

Asn Arg Glu Gly Leu Arg Val Ala Val Ile Val Asn Asp Met Ser Glu
35 40 45

Val Asn Ile Asp Ala Glu Glu Val Gln Arg Asp Val Ala Leu His Arg
50 55 60

Gly Arg Asp Glu Leu Ile Glu Met Ser Asn Gly Cys Ile Cys Cys Thr
65 70 75 80

Leu Arg Ala Asp Leu Leu Glu Gln Ile Ser Met Leu Ala Arg Gln Gln
85 90 95

Arg Phe Asp Tyr Leu Leu Ile Glu Ser Thr Gly Ile Ser Glu Pro Met
100 105 110

Pro Val Ala Glu Thr Phe Ala Phe Leu Asp Ala Asp Gly Phe Ser Leu
115 120 125

Ser Glu Leu Ala Arg Leu Asp Thr Leu Val Thr Val Val Asp Gly Ser
130 135 140

Arg Phe Gln Glu Leu Leu Glu Ser Pro His Thr Val Asp Gln Asp Asp
145 150 155 160

Ala Thr Pro Asp Ala Pro Lys Arg His Leu Ala Asp Leu Leu Ile Glu
165 170 175

Gln Val Glu Tyr Ala Asn Val Ile Leu Val Asn Lys Leu Asp Leu Ile
180 185 190

Asp Ala Ala Gln Tyr Gln Ala Val Gln Ala Ile Leu Thr Gly Leu Asn
195 200 205

Pro Thr Ala Arg Ile Met Pro Met Ala His Gly Asn Ile Pro Ser Ala
210 215 220

Ser Leu Leu Gly Thr His Leu Phe Asp Leu Pro Ser Leu Ala Ala Ser
225 230 235 240

Pro Gly Trp Met Arg Lys Met Glu Ala Ala Asp Ala Pro Ala Ser Glu
245 250 255

Ser Asp Thr Tyr Gly Val Thr Ser Trp Val Tyr Arg Glu Arg Ala Pro
260 265 270

Phe His Pro Gln Arg Leu Leu Asp Phe Leu Gln Gln Pro Trp Cys Asn
275 280 285

Gly Arg Leu Leu Arg Ser Lys Gly Tyr Phe Trp Leu Ala Ser Arg His
290 295 300

Leu Glu Thr Gly Leu Leu Val Gln Ser Gly Lys Arg Phe Gln Trp Asp
305 310 315 320

Tyr Val Gly Arg Trp Trp Asn Phe Ile Glu Pro Ser Gln Trp Pro Arg
325 330 335

Asp Glu Tyr Arg Leu Gln Gly Ile Arg Ala Lys Trp Asp Ser Val Val
340 345 350

Gly Asp Cys Arg Gln Glu Leu Val Phe Ile Gly Gln Gly Leu Asp Thr
355 360 365

Asp Ala Leu Gln Arg Glu Leu Asp His Cys Leu Leu Ser Ala Gln Glu
370 375 380
Ile Ala Ala Gly Pro Leu Ala Trp Gln Ala Leu Pro Gly Ala Thr Ala
385 390 395 400

Phe Asp Arg Gln Thr Leu Ala Arg Pro Pro His Ser Pro Trp Arg Leu
405 410 415

Pro Pro Phe Asp Pro Arg
420

<210> 6
<211> 2371
<212> DNA
<213> Pseudomonas putida

<220>
<221> CDS
<222> (1)..(582)
<223> Coding region of alpha-subunit gene

<220>
<221> CDS
<222> (624)..(1286)
<223> Coding region of beta-subunit gene

<220>
<221> gene
<222> (1283)..(2371)
<223> Gene of activator protein

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atg acg gca act tca acc cct ggt gag cgg gca cgc gca ttg ttt gca 48
Met Thr Ala Thr Ser Thr Pro Gly Glu Arg Ala Arg Ala Leu Phe Ala
1 5 10 15

gtg ctc aag cgc aaa gac ctc atc ccc gag ggc tac atc gaa cag ctc 96
Val Leu Lys Arg Lys Asp Leu Ile Pro Glu Gly Tyr Ile Glu Gln Leu
20 25 30

acc cag ctg atg gaa cac ggc tgg agc ccg gaa aac ggc gcg cgc atc 144
Thr Gln Leu Met Glu His Gly Trp Ser Pro Glu Asn Gly Ala Arg Ile
35 40 45

gtc gcc aag gcc tgg gtc gat ccg cag ttt cgc gag ctg ctg ctc aag 192
Val Ala Lys Ala Trp Val Asp Pro Gln Phe Arg Glu Leu Leu Lys
50 55 60

gac ggt acg gcc gcc tgc gcc cag ttc ggc ttc acc ggc cca caa ggc 240
Asp Gly Thr Ala Ala Cys Ala Gln Phe Gly Phe Thr Gly Pro Gln Gly
65 70 75 80

gaa tac atc gtc gcc ctg gaa gac acc ccg cag ttg aaa aac gtg atc 288
Glu Tyr Ile Val Ala Leu Glu Asp Thr Pro Gln Leu Lys Asn Val Ile
85 90 95

gtc tgt agc ctg tgc tcc tgc acg aac tgg ccg gtg ctg ggc ctg cca 336

Val Cys Ser Leu Cys Ser Cys Thr Asn Trp Pro Val Leu Gly Leu Pro			
100	105	110	
cct gag tgg tac aag ggc ttc gag ttc cgt gcg cggttg gtc cgg gag			384
Pro Glu Trp Tyr Lys Gly Phe Glu Phe Arg Ala Arg Leu Val Arg Glu			
115	120	125	
ggg cgc acg gta ttg cgc gag ctg ggc acc gag ttg ccc ggc gac atg			432
Gly Arg Thr Val Leu Arg Glu Leu Gly Thr Glu Leu Pro Gly Asp Met			
130	135	140	
gtg gtc aag gtc tgg gac acc agc gct gaa agc cgc tac ctg gtg ctg			480
Val Val Lys Val Trp Asp Thr Ser Ala Glu Ser Arg Tyr Leu Val Leu			
145	150	155	160
ccg caa cga cca gcg ggc tca gag cat atg agc gaa gag cag ttg cgg			528
Pro Gln Arg Pro Ala Gly Ser Glu His Met Ser Glu Glu Gln Leu Arg			
165	170	175	
caa ctg gtc acc aag gac gtg ctg atc ggc gtc gcc ctg ccc cgc gtt			576
Gln Leu Val Thr Lys Asp Val Leu Ile Gly Val Ala Leu Pro Arg Val			
180	185	190	
ggc tga gcaaggccgc ccaacccat tcaacttccg gagtgttcaa t atg gat ggc			632
Gly		Met Asp Gly	
	195		
ttt cac gat ctc ggc ggt ttc cag ggc ttt ggc aaa gtg ccc cac cgc			680
Phe His Asp Leu Gly Gly Phe Gln Gly Phe Gly Lys Val Pro His Arg			
200	205	210	
atc aac agc ctg agc tac aag cag gtg ttc aag cag gac tgg gaa cac			728
Ile Asn Ser Leu Ser Tyr Lys Gln Val Phe Lys Gln Asp Trp Glu His			
215	220	225	
ctg gcc tac agc ctg atg ttc atc ggc gtc gac cac ctg aac aag ttc			776
Leu Ala Tyr Ser Leu Met Phe Ile Gly Val Asp His Leu Asn Lys Phe			
230	235	240	
agc gtc gac gaa ata cgt cat gcc gtc gaa cgc att gac gtg cgc cag			824
Ser Val Asp Glu Ile Arg His Ala Val Glu Arg Ile Asp Val Arg Gln			
245	250	255	260
cac gtc ggc acc gaa tac tac gaa cgt tat gtg atc gcc act gcc acg			872
His Val Gly Thr Glu Tyr Tyr Glu Arg Tyr Val Ile Ala Thr Ala Thr			
265	270	275	
ctg ctg gtc gaa aca ggc gtc atc acc cag gcc gaa ctg gat gaa gca			920
Leu Leu Val Glu Thr Gly Val Ile Thr Gln Ala Glu Leu Asp Glu Ala			
280	285	290	
ctc ggc tcg cac ttc aag ctg gcc aac ccc gcc cat gcg caa ggg cgt			968
Leu Gly Ser His Phe Lys Leu Ala Asn Pro Ala His Ala Gln Gly Arg			
295	300	305	
gct gca att atc ggg cga gcg cct ttt gaa gtg ggc gat cgg gtc atc			1016
Ala Ala Ile Ile Gly Arg Ala Pro Phe Glu Val Gly Asp Arg Val Ile			
310	315	320	
gta cgc gat gaa tac gtg gcc ggg cat gtg cgc atg cct gca tac gtg			1064
Val Arg Asp Glu Tyr Val Ala Gly His Val Arg Met Pro Ala Tyr Val			

325	330	335	340	
cgc ggc aag caa ggc gta gtg ctg cac cg ^g acc act gaa cag tgg cc ^g				1112
Arg Gly Lys Gln Gly Val Val Leu His Arg Thr Thr Glu Gln Trp Pro				
345	350	355		
ttt ccg gac g ^c att ggc cat ggc gac cag agc gct g ^c cat caa cc ^g				1160
Phe Pro Asp Ala Ile Gly His Gly Asp Gln Ser Ala Ala His Gln Pro				
360	365	370		
acc tac cat gtc gag ttc cgc gtg cg ^g gac ctg tgg ggc gat gcc gca				1208
Thr Tyr His Val Glu Phe Arg Val Arg Asp Leu Trp Gly Asp Ala Ala				
375	380	385		
gac gac ggc ctg gtg gta gac ctg ttc gaa agc tat ctg gac agg				1256
Asp Asp Gly Leu Val Val Asp Leu Phe Glu Ser Tyr Leu Asp Arg				
390	395	400		
gtc gaa agc cc ^g cga gtg gtg cgc gca tga gtgccggcgc ccaggcaggc				1306
Val Glu Ser Pro Arg Val Val Arg Ala				
405	410			
cg ^g ctgccgg tgacggcttc tt ^c aggcttc ctcggcgcag gcaagaccac cctgctcaac				1366
cacatcctgc gcaaccgcca gggcctgaag gtggcggtta tcgtcaatga catgagc ^g ag				1426
gtcaacatcg atgccc ^{cc} ca ggtccagcgc gacgttgcgc tgtatcg ^t gg ccaggatgaa				1486
ttgatagaga tgagcaacgg ctgtatctgc tgcaccctgc gcgc ^{cc} gac ^t gcttgagcag				1546
atcagcgcgc tggcgcgcca gcagcgtt ^c gattacctgt tgatcgagtc caccggatt				1606
tccgagccga tgccagtcgc cgagac ^c ttt gccttctgc acgccaacgg tttcagc ^c tc				1666
agcgaactgg cg ^c ggctgga tacgctgg ^t g acgg ^t gg ^t cg atgcccagcca gttcatggcc				1726
atgctcgact ctccc ^{aa} ac cgtcg ^c gcgg gccgacgtca ccacggatga cagcaggcgc				1786
ccgctggccg atctgctgat cgagcagg ^t tc gagtatgcca atgtgattct ggtcaacaaa				1846
cgcgac ^c tgg tcgacgaggc gcagtaccag gc ^c c ^c tcgagg cagttctgc cgg ^c ctaat				1906
ccaggcgcac agatcctg ^c cc gatgg ^t ggcc ggcaacgtcg ccctgtcgag cgtc ^c ttgg ^t				1966
acccagctgt tcgatttgcc cagc ^c ttg ^c cc gcagcgc ^c cc gctggatgaa acagatggac				2026
g ^c gcacgaca ccccggccgg cgagtcgcag acctatggcg tgacgtcatg ggtgtaccga				2086
g ^c gcgcgc ^c cc cgttccatcc gcaacgcttg cttgattttc tcgccccggcc ctggcgc ^c ac				2146
ggccgtcttc tg ^c gcagcaa aggttatttc tggcttgcca g ^c cc ^c ccac ^c g c ^a aaatcg ^c gc				2206
ttgctgg ^t ac acagcggcca gcagttcaa tggactatg ttggccattg gtggacttc				2266
atcgacacgt cacagtggcc acaggacaag tatcgcttc agggcatcat ggccaagtgg				2326
gacagcatcg tcggcgactg ccgacaggag ctgaaaagct tatga				2371

<210> 7
<211> 193
<212> PRT
<213> Pseudomonas putida

<400> 7

Met Thr Ala Thr Ser Thr Pro Gly Glu Arg Ala Arg Ala Leu Phe Ala
1 5 10 15

Val Leu Lys Arg Lys Asp Leu Ile Pro Glu Gly Tyr Ile Glu Gln Leu
20 25 30

Thr Gln Leu Met Glu His Gly Trp Ser Pro Glu Asn Gly Ala Arg Ile
35 40 45

Val Ala Lys Ala Trp Val Asp Pro Gln Phe Arg Glu Leu Leu Leu Lys
50 55 60

Asp Gly Thr Ala Ala Cys Ala Gln Phe Gly Phe Thr Gly Pro Gln Gly
65 70 75 80

Glu Tyr Ile Val Ala Leu Glu Asp Thr Pro Gln Leu Lys Asn Val Ile
85 90 95

Val Cys Ser Leu Cys Ser Cys Thr Asn Trp Pro Val Leu Gly Leu Pro
100 105 110

Pro Glu Trp Tyr Lys Gly Phe Glu Phe Arg Ala Arg Leu Val Arg Glu
115 120 125

Gly Arg Thr Val Leu Arg Glu Leu Gly Thr Glu Leu Pro Gly Asp Met
130 135 140

Val Val Lys Val Trp Asp Thr Ser Ala Glu Ser Arg Tyr Leu Val Leu
145 150 155 160

Pro Gln Arg Pro Ala Gly Ser Glu His Met Ser Glu Glu Gln Leu Arg
165 170 175

Gln Leu Val Thr Lys Asp Val Leu Ile Gly Val Ala Leu Pro Arg Val
180 185 190

Gly

<210> 8
<211> 220

<212> PRT

<213> Pseudomonas putida

<400> 8

Met Asp Gly Phe His Asp Leu Gly Gly Phe Gln Gly Phe Gly Lys Val
1 5 10 15

Pro His Arg Ile Asn Ser Leu Ser Tyr Lys Gln Val Phe Lys Gln Asp
20 25 30

Trp Glu His Leu Ala Tyr Ser Leu Met Phe Ile Gly Val Asp His Leu
35 40 45

Asn Lys Phe Ser Val Asp Glu Ile Arg His Ala Val Glu Arg Ile Asp
50 55 60

Val Arg Gln His Val Gly Thr Glu Tyr Tyr Glu Arg Tyr Val Ile Ala
65 70 75 80

Thr Ala Thr Leu Leu Val Glu Thr Gly Val Ile Thr Gln Ala Glu Leu
85 90 95

Asp Glu Ala Leu Gly Ser His Phe Lys Leu Ala Asn Pro Ala His Ala
100 105 110

Gln Gly Arg Ala Ala Ile Ile Gly Arg Ala Pro Phe Glu Val Gly Asp
115 120 125

Arg Val Ile Val Arg Asp Glu Tyr Val Ala Gly His Val Arg Met Pro
130 135 140

Ala Tyr Val Arg Gly Lys Gln Gly Val Val Leu His Arg Thr Thr Glu
145 150 155 160

Gln Trp Pro Phe Pro Asp Ala Ile Gly His Gly Asp Gln Ser Ala Ala
165 170 175

His Gln Pro Thr Tyr His Val Glu Phe Arg Val Arg Asp Leu Trp Gly
180 185 190

Asp Ala Ala Asp Asp Gly Leu Val Val Asp Leu Phe Glu Ser Tyr
195 200 205

Leu Asp Arg Val Glu Ser Pro Arg Val Val Arg Ala
210 215 220

<210> 9
 <211> 1089
 <212> DNA
 <213> Pseudomonas putida

<220>
 <221> CDS
 <222> (1)..(1089)
 <223> Coding region of activator protein gene

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1 5 10 15		
ggc ttc ctc ggc gca ggc aag acc acc ctg ctc aac cac atc ctg cgc	96	
Gly Phe Leu Gly Ala Gly Lys Thr Thr Leu Leu Asn His Ile Leu Arg		
20 25 30		
aac cgc cag ggc ctg aag gtg gcg gtt atc gtc aat gac atg agc gag	144	
Asn Arg Gln Gly Leu Lys Val Ala Val Ile Val Asn Asp Met Ser Glu		
35 40 45		
gtc aac atc gat gcc gcc cag gtc cag cgc gac gtt gcg ctg tat cgt	192	
Val Asn Ile Asp Ala Ala Gln Val Gln Arg Asp Val Ala Leu Tyr Arg		
50 55 60		
ggc cag gat gaa ttg ata gag atg agc aac ggc tgt atc tgc tgc acc	240	
Gly Gln Asp Glu Leu Ile Glu Met Ser Asn Gly Cys Ile Cys Cys Thr		
65 70 75 80		
ctg cgc gcc gac ctg ctt gag cag atc agc gcg ctg gcg cgc cag cag	288	
Leu Arg Ala Asp Leu Leu Glu Gln Ile Ser Ala Leu Ala Arg Gln Gln		
85 90 95		
cgt ttc gat tac ctg ttg atc gag tcc acc ggg att tcc gag ccg atg	336	
Arg Phe Asp Tyr Leu Leu Ile Glu Ser Thr Gly Ile Ser Glu Pro Met		
100 105 110		
cca gtc gcc gag acc ttt gcc ttt ctc gac gcc aac ggt ttc agc ctc	384	
Pro Val Ala Glu Thr Phe Ala Phe Leu Asp Ala Asn Gly Phe Ser Leu		
115 120 125		
agc gaa ctg gcg cgg ctg gat acg ctg gtg acg gtg gtc gat gcc agc	432	
Ser Glu Leu Ala Arg Leu Asp Thr Leu Val Thr Val Val Asp Ala Ser		
130 135 140		
cag ttc atg gcc atg ctc gac tct ccc gaa acc gtc gcg cgg gcc gac	480	
Gln Phe Met Ala Met Leu Asp Ser Pro Glu Thr Val Ala Arg Ala Asp		
145 150 155 160		
gtc acc acg gat gac agc agg cgc ccgtc gac ggt ctg ctg atc gag	528	
Val Thr Thr Asp Asp Ser Arg Arg Pro Leu Ala Asp Leu Leu Ile Glu		
165 170 175		
cag gtc gag tat gcc aat gtg att ctg gtc aac aaa cgc gac ctg gtc	576	
Gln Val Glu Tyr Ala Asn Val Ile Leu Val Asn Lys Arg Asp Leu Val		
180 185 190		

gac gag gcg cag tac cag gcc ctg cag gca gtt ctc gcc ggg ctc aat	624
Asp Glu Ala Gln Tyr Gln Ala Leu Gln Ala Val Leu Ala Gly Leu Asn	
195 200 205	
cca ggc gca cag atc ctg ccg atg gtg gcc ggc aac gtc gcc ctg tcg	672
Pro Gly Ala Gln Ile Leu Pro Met Val Ala Gly Asn Val Ala Leu Ser	
210 215 220	
agc gtc ctt ggt acc cag ctg ttc gat ttg ccc agc ctt gcc gca gcg	720
Ser Val Leu Gly Thr Gln Leu Phe Asp Leu Pro Ser Leu Ala Ala Ala	
225 230 235 240	
ccc ggc tgg atg aaa cag atg gac gcg cac gac acc ccg gcc ggc gag	768
Pro Gly Trp Met Lys Gln Met Asp Ala His Asp Thr Pro Ala Gly Glu	
245 250 255	
tcg cag acc tat ggc gtg acg tca tgg gtg tac cga gcg cgc gcc ccg	816
Ser Gln Thr Tyr Gly Val Thr Ser Trp Val Tyr Arg Ala Arg Ala Pro	
260 265 270	
ttc cat ccg caa cgc ttg ctt gat ttt ctc gcc cgcc ccc tgg cgc gac	864
Phe His Pro Gln Arg Leu Leu Asp Phe Leu Ala Arg Pro Trp Arg Asp	
275 280 285	
ggc cgt ctt ctg cgc agc aaa ggt tat ttc tgg ctt gcc agc cgc cac	912
Gly Arg Leu Leu Arg Ser Lys Gly Tyr Phe Trp Leu Ala Ser Arg His	
290 295 300	
cgc gaa atc ggc ttg ctg gta cac agc ggc cag cag ttt caa tgg gac	960
Arg Glu Ile Gly Leu Leu Val His Ser Gly Gln Gln Phe Gln Trp Asp	
305 310 315 320	
tat gtt ggc cat tgg tgg aac ttc atc gac acg tca cag tgg cca cag	1008
Tyr Val Gly His Trp Trp Asn Phe Ile Asp Thr Ser Gln Trp Pro Gln	
325 330 335	
gac aag tat cgc ttg cag ggc atc atg gcc aag tgg gac agc atc gtc	1056
Asp Lys Tyr Arg Leu Gln Gly Ile Met Ala Lys Trp Asp Ser Ile Val	
340 345 350	
ggc gac tgc cga cag gag ctg aaa agc tta tga	1089
Gly Asp Cys Arg Gln Glu Leu Lys Ser Leu	
355 360	

<210> 10
<211> 362
<212> PRT
<213> Pseudomonas putida

<400> 10

Met Ser Ala Gly Ala Gln Ala Gly Arg Leu Pro Val Thr Val Leu Ser	
1 5 10 15	

Gly Phe Leu Gly Ala Gly Lys Thr Thr Leu Leu Asn His Ile Leu Arg	
20 25 30	

Asn Arg Gln Gly Leu Lys Val Ala Val Ile Val Asn Asp Met Ser Glu

35

40

45

Val Asn Ile Asp Ala Ala Gln Val Gln Arg Asp Val Ala Leu Tyr Arg
50 55 60

Gly Gln Asp Glu Leu Ile Glu Met Ser Asn Gly Cys Ile Cys Cys Thr
65 70 75 80
Leu Arg Ala Asp Leu Leu Glu Gln Ile Ser Ala Leu Ala Arg Gln Gln
85 90 95

Arg Phe Asp Tyr Leu Leu Ile Glu Ser Thr Gly Ile Ser Glu Pro Met
100 105 110

Pro Val Ala Glu Thr Phe Ala Phe Leu Asp Ala Asn Gly Phe Ser Leu
115 120 125

Ser Glu Leu Ala Arg Leu Asp Thr Leu Val Thr Val Val Asp Ala Ser
130 135 140

Gln Phe Met Ala Met Leu Asp Ser Pro Glu Thr Val Ala Arg Ala Asp
145 150 155 160

Val Thr Thr Asp Asp Ser Arg Arg Pro Leu Ala Asp Leu Leu Ile Glu
165 170 175

Gln Val Glu Tyr Ala Asn Val Ile Leu Val Asn Lys Arg Asp Leu Val
180 185 190

Asp Glu Ala Gln Tyr Gln Ala Leu Gln Ala Val Leu Ala Gly Leu Asn
195 200 205

Pro Gly Ala Gln Ile Leu Pro Met Val Ala Gly Asn Val Ala Leu Ser
210 215 220

Ser Val Leu Gly Thr Gln Leu Phe Asp Leu Pro Ser Leu Ala Ala Ala
225 230 235 240

Pro Gly Trp Met Lys Gln Met Asp Ala His Asp Thr Pro Ala Gly Glu
245 250 255

Ser Gln Thr Tyr Gly Val Thr Ser Trp Val Tyr Arg Ala Arg Ala Pro
260 265 270

Phe His Pro Gln Arg Leu Leu Asp Phe Leu Ala Arg Pro Trp Arg Asp
275 280 285

Gly Arg Leu Leu Arg Ser Lys Gly Tyr Phe Trp Leu Ala Ser Arg His
290 295 300

Arg Glu Ile Gly Leu Leu Val His Ser Gly Gln Gln Phe Gln Trp Asp
305 310 315 320

Tyr Val Gly His Trp Trp Asn Phe Ile Asp Thr Ser Gln Trp Pro Gln
325 330 335
Asp Lys Tyr Arg Leu Gln Gly Ile Met Ala Lys Trp Asp Ser Ile Val
340 345 350

Gly Asp Cys Arg Gln Glu Leu Lys Ser Leu
355 360

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer 1F

<400> 11
ctccaccata tgagtagc tacttcaacg 30

<210> 12
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer 1R

<400> 12
tttcataagg ttcttatctcg gatcaaatgg 30

<210> 13
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer 2F

<400> 13
atgacggcaa cttcaacccc tggtg 25

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer 2R

<400> 14
tcagctcctg tcggcagtgc

20